

*ClustalW Results*[Sequences](#)[Help](#)[Retrieval](#)[BLAST2](#)[FASTA](#)[ClustalW](#)[GCC Assembly](#)[Phrap](#)[Translation](#)

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- PF-0622-USN_SEQ_ID_NO:9
- gi_4165017_ACSS3_Minekura_et_al.

CLUSTAL W (1.7) Multiple Sequence Alignments

Sequence format is Pearson

Sequence 1: PF-0622-USN_SEQ_ID_NO_9 4027 bp

Sequence 2: gi_4165017_ACSS3_Minekura_et_al. 2905 bp

Start of Pairwise alignments

Aligning...

Sequences (1:2) Aligned. Score: 99

Start of Multiple Alignment

There are 1 groups

Aligning...

Group 1: Sequences: 2 Score: 54880

Alignment Score 19234

CLUSTAL-Alignment file created [baaFPaqZw.aln]

CLUSTAL W (1.7) multiple sequence alignment

PF-0622-USN_SEQ_ID_NO_9 GCGCCGGCTGCGACACTGCAGTTGTCTACGCGGCCGGGCCGGACGAG
gi_4165017_ACSS3_Minekura_et_al. -----PF-0622-USN_SEQ_ID_NO_9 GAGGCCTTGGACGGGGTCGCATACGTTCGTCCCTCGCATTGGGGCCCG
gi_4165017_ACSS3_Minekura_et_al. -----PF-0622-USN_SEQ_ID_NO_9 ACAGCTGCGCCAGGATCCCCGGCGGCCGGCGGGCGTGAACGCTCTGG
gi_4165017_ACSS3_Minekura_et_al. -----PF-0622-USN_SEQ_ID_NO_9 GGCTCAGCCAGGCCTGCGCGGGCCCGATGCCGGAGGAACCCGGACTCCGG
gi_4165017_ACSS3_Minekura_et_al. -----PF-0622-USN_SEQ_ID_NO_9 CGTAGCGGTTTGACACAAGGGCGCATATCTTCAAAGCACCTAGTACCTC
gi_4165017_ACSS3_Minekura_et_al. -----PF-0622-USN_SEQ_ID_NO_9 CTACCATTGTCAACTGATAACAGAATTGTTGGGAAGGACTGGGGAAA
gi_4165017_ACSS3_Minekura_et_al. -----GAATTGTTGGGAAGGACTGGGGAAA

PF-0622-USN_SEQ_ID_NO_9
gi_4165017_AC3_Minekura_et_al

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CAGCTGTAACATTCGCCACCCCTCAGAACGCTGCTGGTCTGTGTCACACCA

CCTTAGCCTCTTGATCGAGGAAGATTCTCGCTGAAGTCTGTTAATTCTAC
CCTTAGCCTCTTGATCGAGGAAGATTCTCGCTGAAGTCTGTTAATTCTAC

TTTTGAGTACTTATGAATAACCACGTGCTTCAAAACCATCTACCATGA
TTTTGAGTACTTATGAATAACCACGTGCTTCAAAACCATCTACCATGA

AGCTAAAACATACCATCAACCCATTCTTTATATTTATACATTTCTA
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GTCAAGACAAGAAAAATCAAACCGAATTAAAGCAAAGCCTGTAATTCAA

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TCTCCTGTTGTGTTCCGGCTCCACTTCTGCAACCACGCAGCGATTCA
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TCTGCTGGGCTGGAACAAATTCCGAAGTGTGGACTACAATACTGGCAG

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ATCTTGAAAAAA-----
***** * *

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--AAAAAAA-----
* ***** * *

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AGGCAAAATCAAAAAAAAAAAAAAGG

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